

FIGURE 1

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGCTTCAGCCTGA
AGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCTCTTGGCCTCCAACCTTGTGGG
CTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCATGCTGCTCCCCAGCTGGAAAAACAAGTTCTTA
TGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGG
CATCACCCAGTGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGATGGT
GACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGA
ATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGGAGGCCTCCTGGGATTCAATCC
TGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGAT
TGGAGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCCTG
CTCATCCCAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAG
GCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGG
CCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACC
ACTGGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCT
GCTCCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCATTCCCTTAAGCCAGGACTCAGAGGATCCCTTTG
CCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCCTGACTGACCCTCTGTGATCAAAGA
CCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCAT
TGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTATG
ACTCCACAGTGTCCAGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCA
GGATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 2

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGGGCCT
CCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCTCCTGCTGC
CTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGTTACAGGATCCTG
ACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAA
AGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGGTGA
TTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAGCTGTGTGACGGAGAGC
TGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGCAGTCCGCC
TCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCACAGGGAAGTGGTTCTCTGCCTGTTTCGACAAC
TCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGG
ATCTGGATGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAAGTCAAGTGGGCCCTGTCTCTCAG
GCTCCCTGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGG
CCTCTGTGGATTCTTGGCCTTGGCAGGTCAGCATCCAGTACGACAAAACAGCACGTCTGTGGAGGGAGCATCCTGG
ACCCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAG
GCTCAGACAAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACC
CCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGCCCCATCTGTC
TGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATG
GAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCAATTGACAGCACACGGTGCAATGCAGACGATG
CGTACCAGGGGGGAAGTACCGAGAAGATGATGTGTGCAGGCATCCCGGAAGGGGGTGTGGACACCTGCCAGGGTG
ACAGTGGTGGGCCCCCTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCG
GGGGCCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTG
AGCTGTAATGCTGCTGCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCTGGGGATCCCCCAA
AGTCAGACACAGAGCAAGAGTCCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCATTTCTTGGAGCAGCAAAG
GGCCTCAATTCTGTAAAGAGACCCTCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACAC
TTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGG
AACTTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAGCCAGATCACTGTGGCTGGAGAGGAGAAGG
AAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTACTAGAGCAAGAAACCAGTTGTAATATAA
AATGCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCATTGTTATTACAGCTATGGCCACTATTA
TTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAA

FIGURE 3

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGCTTCCCTGGGG
CAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTGGCTTTGGT
ATTTCAGGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGC
TGCACTTTTGAACCTGACATCAAACCTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTC
CATGAGTTCAAAGAAGGCAAAGATGAGCTGTGCGGAGCAGGATGAAATGTTTCAAGAGCCGGACAGCAGTGTTTGCT
GATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGT
TATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGGAAGTG
AATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGGTC
TGGGCATCCCAAGTTGACCAGGGAGCCAACCTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAAT
GTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAAAATGAC
ATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAAC
TCAAAGGCTTCTCTGTGTGTCTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATG
CTAAAATAATGTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAG
AGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAAGACATATTA
GAAGTTGGGAAAATAATTCATGTGAACTAGACAAGTGTGTTAAGAGTGATAAGTAAAATGCACGTGGAGACAAGT
GCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTG
TCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCCCTGGAAAGTCTATCCCAACATATCCA
CATCTTATATTCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAG
GGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACCTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTC
CCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGTCGGGGACACCGATTT
TATAAATAAACTGAGCACCTTCTTTTAAACAAA
AAAAAAA

FIGURE 4

TGCCGGGCTGCGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGGCTCCACTCGTCTGCCCCTGGACTCCC
GTCTCCTCCTGTCCTCCGGCTTCCCAGAGCTCCCTCCTTATGGCAGCAGCTTCCCGCGTCTCCGGCGCAGCTTCT
CAGCGGACGACCCCTCTCGCTCCGGGGCTGAGCCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGCGGG
TTTGGCTGCTGCTTCCCCGCCGGGTGCCACTGCCACCGCCGCCCTCTGCTGCCGCCGTCCGCGGGATGCTCAG
TAGCCCGCTGCCCCGGCCCCCGGATCCTGTGTTCCCTCGGAAGCCGTTTGCTGCTGCAGAGTTGCACGAAGTAGTC
ATGGCTGCTGTTGGGAGTCCCCGCCGGCAGTGCAGCAGCTGGACACTTTGCGAGGGCTTTTGCTGGCTGCTGCTGCTG
CCCCTCATGCTACTCATCGTAGCCCGCCGGTGAAGCTCGCTGCTTTCCCTACCTCCTTAAGTGAAGTGCACAAACG
CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTTCCCTCTGTGACACCAACACCTGTAAA
TTTGATGGGGAATGTTTAAGAATTGGAGACACTGTGACTTGCGTCTGTCAGTTCAAGTGCAACAATGACTATGTG
CCTGTGTGTGGCTCCAATGGGGAGAGCTACCAGAATGAGTGTACCTGCGACAGGCTGCATGCAAACAGCAGAGT
GAGATACTTGTGGTGTGTCAGAAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGC
TCTGGAGAACTAGTCAAAAGGAGACATCCACCTGTGATATTTGCCAGTTTGGTGCAGAATGTGACGAAGATGCC
GAGGATGTCTGGTGTGTGTGTAATATTGACTGTTCTCAAACCAACTTCAATCCCCTCTGCGCTTCTGATGGGAAA
TCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGTGAGAAACAGGAGAAAATTGAAGTCATGTCTTTGGGT
CGATGTCAAGATAACACAACACTACAACACTAAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCAGAGAAT
GCTAACAAATTAGAAGAAAGTGCCAGAGAACACCACATACCTTGTCCGGAACATTACAATGGCTTCTGCATGCAT
GGGAAGTGTGAGCATTCTATCAATATGCAGGAGCCATCTTGCGAGGTGTGATGCTGGTTATACTGGACAACACTGT
GAAAAAAGGACTACAGTGTCTATACGTTGTTCCCGGTCTGTACGATTTAGTATGTCTTAATCGCAGCTGTG
ATTGGAACAATTAGATTGCTGTGTCATCTGTGTGGTGGTCCCTCTGCATCACAAGGAAATGCCCCAGAAGCAACAGA
ATTCACAGACAGAAGCAAAATACAGGGCACTACAGTTCAGACAATACAACAAGAGCGTCCACGAGGTTAATC**TAA**
AGGGAGCATGTTTCACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATACAGTATTATAGACAAAAGAATAA
GACAAGAGATCTACACATGTTGCCTTGCAATTTGTGGTAATCTACACCAATGAAAACATGTACTACAGCTATATTT
GATTATGTATGGATATATTTGAAATAGTATACATTGTCTTGATGTTTTTCTGTAATGTAAATAAACTATTTATA
TCACACAATATAGTTTTTTCTTTCCCATGTATTTGTTATATATAATAAAATACTCAGTGATGAG

FIGURE 5

TTCTGCTATAGAGATGGAACAGTATATGGAAAGCTCCCAAGAAAGTGAAGAGAGGAAATTGGAAAATTGTGAGTG
GACCTTCTGATACTGCTCCTCCTTGCCTGGAAAAGGGGAAAGAACTGCATGCATATTATTTCAGCGTCCTATATTC
AAAGGATATTCTTGGTGATCTTGGAAAGTGTCCGTATCATGGAATCAATCTCTATGATGGGAAGCCCTAAGAGCCT
TAGTGAACTTGTTTTACCTAATGGCATAAATGGTATCAAAGATGCAAGGAAGGTCACTGTAGGTGTGATTGGAAG
TGGAGATTTTGCCAAATCCTTGACCATTGCACTTATTAGATGCGGCTATCATGTGGTCATAGGAAGTAGAAATCC
TAAGTTTGCTTCTGAATTTTTTCCTCATGTGGTAGATGTCACTCATCATGAAGATGCTCTCACAAAAACAAATAT
AATATTTGTTGCTATACACAGAGAACATTATACCTCCCTGTGGGACCTGAGACATCTGCTTGTGGGTAAAATCCT
GATTGATGTGAGCAATAACATGAGGATAAACAGTACCCAGAATCCAATGCTGAATATTTGGCTTCATTATTCCT
AGATTCTTTGATTGTCAAAGGATTTAATGTTGTCTCAGCTTGGGCACTTCAGTTAGGACCTAAGGATGCCAGCCG
GCAGGTTTATATATGCAGCAACAATATTCAAGCGCGACAACAGGTTATTGAACTTGCCCCGCCAGTTGAATTTTCAT
TCCCATTGACTTGGGATCCTTATCATCAGCCAGAGAGATTGAAAATTTACCCCTACGACTCTTTACTCTCTGGAG
AGGGCCAGTGGTGGTAGCTATAAGCTTGGCCACATTTTTTTTCTTTTATTCCTTTGTGAGAGATGTGATTCATCC
ATATGCTAGAAACCAACAGAGTGACTTTTACAAAATTCCTATAGAGATTGTGAATAAAACCTTACCTATAGTTGC
CATTACTTTGCTCTCCCTAGTATACCTTGCAAGTCTTCTGGCAGCTGCTTATCAACTTTATTACGGCACCAAGTA
TAGGAGATTTCCACCTTGGTTGGAAACCTGGTTACAGTGTAGAAAACAGCTTGGATTACTAAGTTTTTTCTTCGC
TATGGTCCATGTTGCCTACAGCCTCTGCTTACCGATGAGAAGGTGAGAGAGATATTTGTTTCTCAACATGGCTTA
TCAGCAGGTTTCATGCAAATATTGAAAACCTCTTGGAAATGAGGAAGAAGTTTGGAGAATTGAAATGTATATCTCCTT
TGGCATAATGAGCCTTGGCTTACTTTCCCTCCTGGCAGTCACTTCTATCCCTTCAGTGAGCAATGCTTTAAACTG
GAGAGAATTCAGTTTTATTTCAGTCTACACTTGGATATGTGCTCTGCTCATAAGTACTTTCCATGTTTTAATTTA
TGGATGGAAACGAGCTTTTGAGGAAGAGTACTACAGATTTTATACACCACCAAACCTTTGTTCTTGCTCTTGTTTT
GCCCTCAATTGTAATTCTGGATCTTTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAAGTGAATTTGTCTTCC
TATTGACTCTACTTCTTTAAAAGCGGCTGCCCATTACATTCCTCAGCTGTCTTGCAGTTAGGTGTACATGTGAC
TGAGTGTGGCCAGTGAGATGAAGTCTCCTCAAAGGAAGGCAGCATGTGTCCTTTTTCATCCCTTCATCTTGCTG
CTGGGATTGTGGATATAACAGGAGCCCTGGCAGCTGTCTCCAGAGGATCAAAGCCACACCCAAAGAGTAAGGCAG
ATTAGAGACCAGAAAGACCTTGACTACTTCCCTACTTCCACTGCTTTTTTCTGCATTTAAGCCATTGTAAATCTG
GGTGTGTTACATGAAGTGAAAATTAATTCTTTCTGCCCTTCAGTTCTTTATCCTGATACCATTTAAACTGTCTG
AATTAAGTAGACTGCAATAATTCTTTCTTTTGAAAGCTTTTAAAGGATAATGTGCAATTCACATTAATAATTGATT
TTCCATTGTCAATTAGTTATACTCATTTTCTGCCTTGATCTTTTATTAGATATTTTGTATCTGCTTGGAAATATA
TTATCTTCTTTTTAACTGTGTAATTGGTAATTACTAAAACCTCTGTAATCTCCAAAATATTGCTATCAAATTACAC
ACCATGTTTTCTATCATCTCATAGATCTGCCTTATAAACATTTAAATAAAAAGTACTATTTAATGATTTAACTT
CTGTTTTGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 6

MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCIDIYSTLLGLPA
DIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRDFYSP
LVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQRNRSNYDAYQAQPLATRSSPRPGQPPKVKSEFNYS
ITGYV

Signal sequence.

amino acids 1-24

Transmembrane domains.

amino acids 82-102, 120-140, 160-180

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 216-224

N-myristoylation sites.

amino acids 17-22, 20-25, 60-65, 101-106, 128-133, 167-172, 178-183

PMP-22/EMP/MP20/Claudin family.

amino acids 4-181

FIGURE 7

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYYFLCGQPLHFIPRKQ
LCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDNFTEALAETACRQMGYSRAVE
IGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSLKTPRVVGGEESVDSWPWQVSIQYDKQHVC
GGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKLGSFPSLAVAKIIIEFNPMYPKDNDIALMKLQFPLTFSGT
VRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAAYQGEVTEKMMCAGIPEGGV
DTCQGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain.

amino acids 33-60

Trypsin.

amino acids 200-424

Kringle domain proteins.

amino acids 225-242, 376-388

Apple domain proteins.

amino acids 199-239, 196-236, 237-270, 298-328, 368-401, 367-400, 403-430

LDL-receptor class A.

amino acids 70-89

CUB domain proteins.

amino acids 397-406

FIGURE 8

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIIITSKGKGNANLEYKTGAF
SMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLYNVTINNTYSC
MIENDIAKATGDIKVTETSEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

Signal peptide.

amino acids 1-28

Transmembrane domain.

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220, 220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

Immunoglobulin domain.

amino acids 49-132

FIGURE 9

MVLWESPRQCSSWTLCGEFCWLLLLPVMLLIVARPVKLAAPFPTSLSDCQTPTGWNC SGYDDRENDLFLCDTNTCK
FDGECLRIGDTVTCVCQFKCNNDYVPVCGSNGESYQNECYLRQAACKQQSEILVVSEGSCATDAGSGSGDGVHEG
SGETSQKETSTCDICQFGAECDEDAEDVWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLG
RCQDNTTTTTTTSKEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRC DAGYTGQHC
EKKDYSVLYVVP GPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRQKQNTGHYSSDNTTRASTRLI

N-glycosylation sites.

amino acids 55-58, 230-233, 365-368

Glycosaminoglycan attachment sites.

amino acids 141-144, 143-146

Tyrosine kinase phosphorylation site.

amino acids 236-242

N-myristoylation sites.

amino acids 133-138, 140-145, 142-147, 146-151, 150-155

EGF-like domain cysteine pattern signature.

amino acids 289-301

Kazal-type serine protease inhibitor domain.

amino acids 91-135, 182-227

FIGURE 10

MESISMMGSPKSLSETCLPNGINGIKDARKVTVGVIGSGDFAKSLTIRLIRCGYHVVIGSRNPKFASEFFPHVVD
VTHHEDALTKTNIIFVAIHREHYTSLWDLRHLLVGKILIDVSNNMRINQYPESNAEYLASLFPDSLIVKGFNVVS
AWALQLGPKDASRQVYICSNNIQARQQVIELARQLNFIPIDLGSLSAREIENLPLRLFTLWRGPVVVAISLATF
FFLYSFVRDVIHPYARNQQSDFYKIPIEIVNKTLPPIVAITLLSLVYLAGLLAAAYQLYYGTKYRRFPPWLETWLQ
CRKQLGLLSFFFAMVHVAYSCLPMRRSERYLFLNMAYQQVHANIENSWNEEEVWRIEMYISFGIMSLGLLSLLA
VTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKRAFEEEYYRFYTPPNFVLALVLPISIVILDLLQLC
RYPD

Transmembrane domains.

amino acids 210-230, 257-277, 299-319, 359-379, 393-413, 428-448

N-glycosylation site.

amino acids 256-259

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 29-32

Tyrosine kinase phosphorylation site.

amino acids 416-424

N-myristoylation sites.

amino acids 8-13, 24-29, 34-39, 193-198, 274-279